

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2001, 11:06:20 ; Search time 53.94 Seconds
(without alignments)
7.644 Million cell updates/sec

Title: US-09-328-296-8

Perfect score: 37

Sequence: 1 TGYIYH 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.*
2: PIR.*
3: PIR.*
4: PIR.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	104	2	Ig heavy chain V r
2	37	100.0	105	2	Ig heavy chain var
3	37	100.0	120	2	Ig heavy chain V r
4	36	97.3	108	2	Ig heavy chain V r
5	35	94.6	126	2	Ig heavy chain V r
6	34	91.9	98	2	Ig heavy chain V r
7	34	91.9	98	2	Ig heavy chain V r
8	34	91.9	105	2	Ig heavy chain V r
9	34	91.9	107	2	Ig heavy chain V r
10	34	91.9	109	2	Ig heavy chain V r
11	34	91.9	110	2	Ig heavy chain V r
12	34	91.9	117	1	Ig heavy chain V r
13	34	91.9	117	2	Ig heavy chain V r
14	34	91.9	118	2	Ig heavy chain V r
15	34	91.9	129	2	Ig heavy chain V r
16	34	91.9	135	2	Ig heavy chain V r
17	33	89.2	131	2	Ig heavy chain V r
18	33	89.2	524	2	Ig heavy chain V r
19	32	86.5	182	2	Ig heavy chain V r
20	32	86.5	221	2	Ig heavy chain V r
21	32	86.5	361	2	Ig heavy chain V r
22	32	86.5	416	2	Ig heavy chain V r
23	32	86.5	421	2	Ig heavy chain V r
24	32	86.5	421	2	Ig heavy chain V r
25	32	86.5	629	2	Ig heavy chain V r
26	32	86.5	747	2	Ig heavy chain V r
27	31	83.8	104	2	Ig heavy chain V r
28	31	83.8	112	2	Ig heavy chain V r
29	31	83.8	117	2	Ig heavy chain V-D

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30	31	83.8	126	2	S58121	Ig heavy chain V r
31	31	83.8	138	2	S21810	Ig heavy chain V r
32	31	83.8	232	2	T16258	Ig heavy chain V r
33	31	83.8	288	2	A05235	Ig heavy chain V r
34	31	83.8	307	2	E83093	Ig heavy chain V r
35	31	83.8	311	2	D69229	Ig heavy chain V r
36	31	83.8	347	2	F22845	Ig heavy chain V r
37	31	83.8	369	2	A72453	Ig heavy chain V r
38	31	83.8	449	2	T16259	Ig heavy chain V r
39	31	83.8	451	2	T24018	Ig heavy chain V r
40	31	83.8	460	2	T48061	Ig heavy chain V r
41	31	83.8	461	2	T01300	Ig heavy chain V r
42	31	83.8	520	2	F82798	Ig heavy chain V r
43	31	83.8	522	2	T41604	Ig heavy chain V r
44	31	83.8	590	2	A26638	Ig heavy chain V r
45	31	83.8	643	1	FOV2ZW	Ig heavy chain V r

ALIGNMENTS

RESULT 1

Ig heavy chain V region (clone RFT57H), rheumatoid factor - human

C:Species: Homo sapiens (man)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S69899

Eur. J. Immunol. 23, 1220-1225, 1993

A:Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune re

A:Reference number: S69896; MUID:93272805

A:Accession: S69899

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-104 <RAN>

A:Cross-references: EMBL:234893; NID:9509803; PIDN:CA84376.1; PID:9509804

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

F:15-98/Domain: Immunoglobulin homology <IMX>

Query Match 100.0%; Score 37; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYIYH 6
Db 30 TGYIYH 35

RESULT 2

Ig heavy chain variable region, subgroup I (clone MH52) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 30-May-1997

C:Accession: S67941

R:Hexham, J.M.; Furmanak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

Autoimmunity 12, 135-141, 1992

A:Title: Cloning of a human autoimmune response: preparation and sequencing of a huma

A:Reference number: S67940; MUID:92314301

A:Accession: S67941

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-105 <HEX>

A:Cross-references: EMBL:X73851

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

Query Match 100.0%; Score 37; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYIYH 6
|||||

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OM protein - protein search, using sw model

Run on: May 8, 2001 11:06:21 ; Search time 53.94 Seconds
(without alignments)
5.096 Million cell updates/sec

Title: US-09-328-296-10

Sequence: 1 EGIV 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_67:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	15	2 A61522	7.5k surfactant-as
2	22	100.0	57	2 S66314	Protein kinase AKI
3	22	100.0	72	2 E69828	hypothetical prote
4	22	100.0	76	2 S38554	tec protein - phag
5	22	100.0	81	2 F69430	hypothetical prote
6	22	100.0	83	2 H82778	hypothetical prote
7	22	100.0	96	2 E70913	probable ribosomal
8	22	100.0	96	2 T36593	hypothetical prote
9	22	100.0	106	2 H64345	hypothetical prote
10	22	100.0	106	2 T29983	hypothetical prote
11	22	100.0	107	2 S78532	hypothetical prote
12	22	100.0	114	2 A72734	MTCF-1 protein SPL
13	22	100.0	120	2 T18158	hypothetical prote
14	22	100.0	129	2 F75076	hypothetical prote
15	22	100.0	132	2 T13178	hypothetical prote
16	22	100.0	139	2 A41404	repressor protein
17	22	100.0	139	2 S38808	cathepsin L (EC 3.
18	22	100.0	143	2 G83830	1g heavy chain - m
19	22	100.0	143	2 T41630	hypothetical prote
20	22	100.0	143	2 B39061	very hypothetical
21	22	100.0	145	2 I39505	protein-tyrosine k
22	22	100.0	145	2 I39502	gene aac(6')-I ^K pr
23	22	100.0	145	2 H70022	aminoglycoside 6'-
24	22	100.0	146	2 A48897	aminoglycoside NG'
25	22	100.0	146	2 I39504	hypothetical prote
26	22	100.0	147	1 VBHU	gene aac(6')-I ^K pr
27	22	100.0	150	2 S65955	transhyretin prec
28	22	100.0	153	2 S31943	penicillin-binding
29	22	100.0	153	2 C69551	hypothetical prote

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30	22	100.0	153	2 D64628	hypothetical prote
31	22	100.0	154	2 S42254	hypothetical prote
32	22	100.0	157	2 H65203	conserved hypotet
33	22	100.0	157	2 B69538	conserved hypotet
34	22	100.0	160	2 A39061	protein-tyrosine k
35	22	100.0	161	2 E64437	probable dctp deam
36	22	100.0	161	2 S76047	hypothetical prote
37	22	100.0	163	2 H69990	sugar transport pr
38	22	100.0	164	2 S31947	penicillin-binding
39	22	100.0	164	2 S31948	penicillin-binding
40	22	100.0	170	1 A28670	flavodoxin [valida
41	22	100.0	174	2 F71017	hypothetical prote
42	22	100.0	175	2 G75144	hypothetical prote
43	22	100.0	175	2 C71184	hypothetical prote
44	22	100.0	175	2 C75115	hydrogenase relate
45	22	100.0	179	2 T31625	hypothetical prote

ALIGNMENTS

Record 1
A61522
7.5k surfactant-associated protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Oct-1994
C:Accession: A61522
R:Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.; Wong-Chong, M.L.; Gottton, S.A
Exp. Lung Res. 17, 559-567, 1991
A:Title: Identification, isolation, and partial characterization of a 7.5-kDa surfact
A:Reference number: A61522; M01D:91317170
A:Accession: A61522
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <SIN>

Query Match 100.0%; Score 22; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGIV 4
DB 8 EGIV 11
RESULT 2
S66314
protein kinase AKI (EC 2.7.1.-) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
C:Accession: S66314; S58256
R:Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase gene
A:Reference number: S66314; M01D:96123233
A:Accession: S66314
A:Molecule type: DNA
A:Residues: 1-57 <THU>
A:Cross-References: EMBL:X86946; NID:9928885; PIDN:CA60509.1; PID:9928886
C:Genetics:
A:Gene: AKI
A:Introns: 40/2
C:Keywords: ATP; phosphotransferase; protein kinase
F:1-57/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EGIV 4